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<110> Tang, Y. Tom
      Walker, Michael G.
<120> GROWTH-RELATED INFLAMMATORY AND IMMUNE RESPONSE PROTEIN
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                 35
                                      40
His Met Ile Tyr Met Arg Ala Leu Gln Ile Val Tyr Gly Ile Arg
                 50
                                      55
Leu Glu His Phe Tyr Met Met Pro Val Asn Ser Glu Val Met Tyr
                                     70
                 65
Pro His Leu Met Glu Gly Phe Leu Pro Phe Ser Asn Leu Val Thr
                                     85
                 80
His Leu Asp Ser Phe Leu Pro Ile Cys Arg Val Asn Asp Phe Glu
                 95
                                     100
                                                         105
Thr Ala Asp Ile Leu Cys Pro Lys Ala Lys Arg Thr Ser Arg Phe
                110
                                     115
Leu Ser Gly Ile Ile Asn Phe Ile His Phe Arg Glu Ala Cys Arg
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                125
Glu Thr Tyr Met Glu Phe Leu Trp Gln Tyr Lys Ser Ser Ala Asp
                                     145
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Lys Met Gln Gln Leu Asn Ala Ala His Gln Glu Ala Leu Met Lys
                155
                                     160
Leu Glu Arg Leu Asp Ser Val Pro Val Glu Glu Glu Glu Phe
                170
                                     175
Lys Gln Leu Ser Asp Gly Ile Gln Glu Leu Gln Gln Ser Leu Asn
                185
                                     190
Gln Asp Phe His Gln Lys Thr Ile Val Leu Gln Glu Gly Asn Ser
                200
                                     205
Gln Lys Lys Ser Asn Ile Ser Glu Lys Thr Lys Arg Leu Asn Glu
                215
                                     220
Leu Lys Leu Ser Val Val Ser Leu Lys Glu Ile Gln Glu Ser Leu
                230
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Lys Thr Lys Ile Val Asp Ser Pro Glu Lys Leu Lys Asn Tyr Lys

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245
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Glu Lys Met Lys Asp Thr Val Gln Lys Leu Lys Asn Ala Arg Gln
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                                     265
Glu Val Val Glu Lys Tyr Glu Ile Tyr Gly Asp Ser Val Asp Cys
                                     280
                                                          285
                275
Leu Pro Ser Cys Gln Leu Glu Val Gln Leu Tyr Gln Lys Lys Ile
                                                          300
                290
                                     295
Gln Asp Leu Ser Asp Asn Arg Glu Lys Leu Ala Ser Ile Leu Lys
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                                     310
                                                          315
Glu Ser Leu Asn Leu Glu Asp Gln Ile Glu Ser Asp Glu Ser Glu
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                                     325
                                                          330
Leu Lys Lys Leu Lys Thr Glu Glu Asn Ser Phe Lys Arg Leu Met
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                                     340
                                                          345
Ile Val Lys Lys Glu Lys Leu Ala Thr Ala Gln Phe Lys Ile Asn
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Lys Lys His Glu Asp Val Lys Gln Tyr Lys Arg Thr Val Ile Glu
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Asp Cys Asn Lys Val Gln Glu Lys Arg Gly Ala Val Tyr Glu Arg
                380
                                     385
Val Thr Thr Ile Asn Gln Glu Ile Gln Lys Ile Lys Leu Gly Ile
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                                     400
                                                          405
Gln Gln Leu Lys Asp Ala Ala Glu Arg Glu Lys Leu Lys Ser Gln
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Glu Ile Phe Leu Asn Leu Lys Thr Ala Leu Glu Lys Tyr His Asp
                425
                                     430
                                                          435
Gly Ile Glu Lys Ala Ala Glu Asp Ser Tyr Ala Lys Ile Asp Glu
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gcgcgggcag gtgccgggac gctgggcctg gcggtgtttt cgtcgtgctc agcggtggga 240
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tettteecca gatataatgt agetgagatt gtgatteata ttegeaataa gatettaaca 360
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tacatgatgc cagtgaactc tgaagtcatg tatccacatt taatggaagg cttcttacca 540
ttcagcaatt tagttactca tctggactca tttttgccta tctgccgggt gaatgacttt 600
gagactgctg atattctatg tccaaaagca aaacggacaa gtcggttttt aagtggcatt 660
atcaacttta ttcacttcag agaagcatgc cgtgaaacgt atatggaatt tctttggcaa 720
tataaateet etgeggacaa aatgeaacag ttaaaegeeg cacaceagga ggeattaatg 780
aaactggaga gacttgattc tgttccagtt gaagagcaag aagagttcaa gcagctttca 840
gatggaattc aggagctaca acaatcacta aatcaggatt ttcatcaaaa aacgatagtg 900
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<212> DNA

<213> Homo sapiens

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cttaaaaatg ccagacaaga agtggtggag aaatatgaaa tctatggaga ctcagttgac 1140
tgcctgcctt catgtcagtt ggaagtgcag ttatatcaaa agaaaataca ggacctttca 1200
gataataggg aaaaattagc cagtatctta aaggagagcc tgaacttgga ggaccaaatt 1260
gagagtgatg agtcagaact gaagaaattg aagactgaag aaaattcgtt caaaagactg 1320
atgattgtga agaaggaaaa acttgccaca gcacaattca aaataaataa gaagcatgaa 1380
gatgttaagc aatacaaacg cacagtaatt gaggattgca ataaagttca agaaaaaaga 1440
ggtgctgtct atgaacgagt aaccacaatt aatcaagaaa tccaaaaaat taaacttgga 1500
attcaacaac taaaagatgc tgctgaaagg gagaaactga agtcccagga aatatttcta 1560
aacttgaaaa ctgctttgga gaaataccac gacggtattg aaaaggcagc agaggactcc 1620
tatgctaaga tagatgagaa gacagctgaa ctgaagagga agatgttcaa aatgtcaacc 1680
tgattaacaa aattacatgt ctttttgtaa atggcttgcc atcttttaat tttctattta 1740
qaaaqaaaaq ttgaaqcgaa tggaaqtatc agaaqtacca aataatqttg qcttcatcag 1800
tttttataca ctctcataag tagttaataa gatgaattta atgtaggctt ttattaattt 1860
ataattaaaa taacttgtgc agctattcat gtctctactc tgccccttgt tgtaaatagt 1920
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aggtgagcgc gagatgacgg aggaaggaag cctgcagaca gacgccttct ccatcccaag 180
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<221> unsure
<222> 117, 469
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ggaggaagga agcctgcaga cagacgcctt ctccatccca aggcgcgggc aggtgccggg 180
acgctgggcc tggcggtgtt ttcgtcgtgc tcagcggtgg gaggaggcgg aagaaaccag 240
agcctgggag attaacagta aacttccaag atggaaactt tgtctttccc cagatataat 300
gtagctgaga ttgtgattca tattcgcaat aagatcttaa caggagctga tggtaaaaac 360
ctcaccaaga atgatettta tecaaateca aageetgaag tettgeacat gatetacatg 420
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PC-0022 CIP
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cgtcgtgctc agcggtggga ggaggcggaa gaaaccagag cctgggagat taacaggaaa 180
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ttcgcaataa gatcttaaca ggagctgatg gtaaaaacct caccaagaat gatctttatc 300
caaatccaaa gcctgaagtc ttgcacatga tctacatgag agccttacaa atagtctatg 360
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ataatgtagc tgagattgtg attcatattc gcaataagat cttaacagga gctgatggta 180
aaaacctcac caagaatgat ctttatccaa atccaaagcc tgaagtcttg cacatgatct 240
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ttnntgaaaa tcctgattta gtgattgttg tagctcctga attccatctg aaagctgctt 180
qaactettet tgetetteaa etggaacaga ateaagtete teeagtttea ttaatgeete 240
ctggtgtgcg gcgtttaact gttgcatttt gtccgcagag gatttatatt gccaaagaaa 300
ttccatatac gtttcacggc atgcttctct gaagtgaata aagttgataa tgccacttaa 360
aaaccgactt gtccgttttg cttttggacn tagaatatca gcagtctcaa agtcnttcac 420
ccggcagata ggcaaaaatg agtccagatg agtaactaaa ttgctgaatg gtaagaagct 480
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agagggaaat tcccaaaaga agtcaaatat ttcagagaaa accaagcgtt tgaatgaact 180
aaaattgtcg gtggtttctt tgaaagaaat acaagagagt ttgaaaacaa aaattgtgga 240
ttctccagag aagttaaaga attataaaga aaaaatgaaa gatacggtcc agaagcttaa 300
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tcatgtcagt tggaagtgca gttatatcaa aagaaaatac aggacctttc agataatagg 420
gaaaaattag ccagtatctt aaaggagagc ctgaacttgg aggaccaaat tgagagtgat 480
gagtcagaac tgaagaaatt gaagactgaa gaaaattcgt tcaaaagact gatgattgtg 540
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ccagagaagt taaagaatta taaagaaaaa atgaaagata cggtccagaa gcttaaaaat 180
gccagacaag aagtggtgga gaaatatgaa atctatggag actcagttga ctgcctgcct 240
tcatgtcagt tggaagtgca gttatatcaa aagaaaatac aggacctttc agataatagg 300
gaaaaattag ccagtatctt aaaggagagc ctgaacttgg aggaccaaat tgagagtgat 360
gagtcagaac tgaagaaatt gaagactgaa gaaaattcgt tcaaaagact gatgattgtg 420
aagaaggaaa aacttgccac agcacaattc aaaataaata agaagcatga agatgtgtag 480
caatacaaac gcacagtaat tgaggattgc cataaagttc cagaaaaaag aggtgctgtc 540
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PC-0022 CIP
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aattaataaa agcctacatt aaattcatct tattaactac ttatgagagt gtataaaaac 180
tgatgaagcc aacattattt ggtacttctg atacttccat tcgcttcaac ttttctttct 240
aaatagaaaa ttaaaagatg gcaagccatt tacaaaaaga catgtaattt tgttaatcag 300
gttgacattt tgaacatctt cctcttcagt tcagctgtct tctcatctat cttagcatag 360
qaqtcctctq ctqccttttc aataccgtcg tggtatttct ccaaagcagt tttcaagttt 420
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ggttcatatt cgcaataaac tactaacagg agccgatggc aaaaacctct ctaagaatga 180
tctttatcca aacccaaagc ccgatgtctt atacatgatc tacatgagag ccttacaaat 240
agtgtatggg gtccggctgg agcatttcta catgatgcca gtgaacgcag
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tctccaagag cgattttctt ccaaacccga agcctgaagt cctgtacatg atttacatga 240
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catggtcata aaaggacaga gaaccaatgg tacccacgct agttagctga gactgcggtc 180
cttctattag cttcaatata actactccaa acagaaagcg acagcgccgt tttcgggtgg 240
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ttttcaagtc taccaagatt tcctgagact tcagtttctc ccgtttttcg gcgtctctta 420
gctgctgaat cccagattta atcttgtgga tgtcttgatt aatggcggtt acttgctcgc 480
agacagcatc tcttttttct tgaactttat tgcaatctct aaaagggaac agagacacct 540
gacgtaacct ctcttaagca ttttaaaaac cat
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306, 319, 339, 360, 378, 395
<223> unknown or other
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Tyr Met Ile Tyr Met Arg Ala Leu Gln Leu Val Tyr Gly Val Arg
                 50
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Leu Glu His Phe Tyr Met Met Pro Val Asn Ile Glu Val Met Tyr
                                     70
                 65
Pro His Ile Met Glu Gly Phe Leu Pro Val Ser Asn Leu Phe Phe
                 80
                                     85
His Leu Asp Ser Phe Met Pro Ile Cys Arg Val Asn Asp Phe Glu
                 95
                                    100
                                                         105
Ile Ala Asp Ile Leu Tyr Pro Lys Ala Asn Arg Thr Ser Arg Phe
                110
                                    115
                                                         120
Leu Ser Gly Ile Ile Asn Phe Ile His Phe Arg Glu Thr Cys Leu
                125
                                    130
                                                         135
Glu Lys Tyr Glu Glu Phe Leu Leu Gln Asn Lys Ser Ser Val Asp
                140
                                    145
                                                         150
Lys Ile Gln Gln Leu Ser Asn Ala His Gln Glu Ala Leu Met Lys
                155
                                    160
                                                         165
Leu Glu Lys Leu Asn Ser Val Pro Val Glu Glu Glu Glu Phe
                170
                                    175
Lys Gln Leu Lys Asp Asp Ile Gln Glu Leu Gln His Leu Leu Asn
                                    190
                185
Gln Asp Phe Arg Gln Lys Thr Thr Leu Leu Gln Glu Arg Tyr Thr
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205

200

Lys	Met	Lys	Ser	Asp 215	Phe	Ser	Glu	Lys	Thr 220	Lys	His	Val	Asn	Glu 225
Leu	Lys	Leu	Ser	Val 230	Val	Ser	Leu	Lys	Glu 235	Val	Gln	Asp	Ser	Leu 240
Lys	Ser	Lys	Ile	Val 245	Asp	Ser	Pro	Glu	Lys 250	Leu	Lys	Asn	Tyr	Lys 255
Glu	Lys	Met	Lys	Asp 260	Thr	Val	Gln	Lys	Leu 265	Arg	Ser	Ala	Arg	Glu 270
				275	Tyr	_		_	280	_			_	285
Leu	Pro	Ser	Cys	Gln 290	Leu	Glu	Val	Gln	Leu 295	Tyr	Gln	Lys	Lys	Ser 300
	-			305	Asn	_		-	310					315
Glu	Ser	Leu	Asn	Leu 320	Glu	Gly	Gln	Ile	Asp 325	Ser	Asp	Ser	Ser	Glu 330
Leu	Lys	Lys	Leu	Lys 335	Thr	Glu	Glu	Asn	Ser 340	Leu	Ile	Arg	Leu	Met 345
Thr	Leu	Lys	Lys	Glu 350	Arg	Leu	Ala	Thr	Met 355	Gln	Phe	Lys	Ile	Asn 360
_	_			365	Val			_	370					375
				380	Gln				385					390
				395	Gln				400					405
Gln	Gln	Leu	Arg	Asp 410	Ala	Glu	Lys	Arg	Glu 415	Lys	Leu	Lys	Ser	Gln 420
Glu	Ile	Leu	Val	Asp 425	Leu	Lys	Ser	Ala	Leu 430	Glu	Lys	Tyr	His	Glu 435
Gly	Ile	Glu	Lys	Thr 440	Thr	Glu	Glu	Cys	Cys 445	Thr	Arg	Ile	Gly	Gly 450
Lys	Thr	Ala	Glu	Leu 455	Lys	Arg	Arg	Met	Phe 460	Lys	Met	Pro	Pro	